APPENDIX A

```
RESULT 10
; Sequence 338,
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Chen,Jian
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Pan,James
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  APPLICANT:  Zhang,Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  Prior application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 338
;   LENGTH: 368
;   TYPE: PRT
;   ORGANISM: Homo Sapien


  Query Match            95.2%;  Score 1902.5;  DB 14;  Length 368;
  Best Local Similarity  98.6%;  Pred. No. 1e-183;
  Matches  359;  Conservative   1;  Mismatches   3;  Indels  1;  Gaps   1;

Qy        1 MGLLAFLKTQFVLHLLVGFVFVVSGLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQ 60
            |||·|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MGLLAFLKTQFVLHLLVGFVFVVSGLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQ 60

Qy       61 LVMLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKV 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 LVMLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKV 120

Qy      121 LAKKELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRF 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 LAKKELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRF 180

Qy      181 TETKHRVSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSL 240
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 TETKHRVSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSL 240

Qy      241 LGILYGKKYEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFK 300
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 LGILYGKKYEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFK 300

Qy      301 PARRPWTLLNFLSWATILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFGVRRLIGVTE 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 PARRPWTLLNFLSWATILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFGVRRLIG-ES 359

Qy      361 IEKG 364
            :| |
Db      360 LEPG 363
```